

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings of claims in the application.

Listing of Claims:

1. (Currently amended) An isolated polynucleotide sequence comprising SEQ ID NO: 113 comprising a functional vascular tissue-specific *E. grandis* cOMT promoter ~~contained in SEQ ID NO: 113.~~

2. (Currently amended) An isolated polynucleotide sequence comprising a sequence selected from the group consisting of:

(a) SEQ ID NO: 12, SEQ ID NO: 60, nucleotides 1-1643 of SEQ ID NO: 113, nucleotides 1019-1643 of SEQ ID NO: 113; nucleotides 1525-1643 of SEQ ID NO: 113 and their complements[[:]], wherein said sequence comprises a functional vascular tissue-specific *E. grandis* cOMT promoter.

~~(b) reverse complements and reverse sequences of the sequences recited in (a);~~

~~(c) sequences having at least 75% identity to a sequence recited in (a);~~

~~(d) sequences having at least 90% identity to a sequence recited in (a);~~

~~(e) a polynucleotide sequence that is substantially complementary to a sequence in (a) and hybridizes to said sequence under stringent conditions; and~~

~~(f) a polynucleotide comprising a 20-mer, a 40-mer, a 60-mer, an 80-mer, a 100-mer, a 120-mer, a 150-mer, a 180-mer, a 220-mer, a 250-mer, a 300-mer, 400-mer, 500-mer or 600-mer of a sequence recited in (a) or (d) above.~~

3. (Previously presented) A genetic construct comprising a polynucleotide sequence of claim 1 or claim 2.

4. (Currently amended) A genetic construct comprising, in the 5'-3' direction:

(a) a promoter sequence;

(b) a DNA sequence of interest; and

(c) a gene termination sequence,

wherein the promoter sequence comprises ~~a functional vascular tissue-specific *E. grandis* cOMT promoter contained in SEQ ID NO: 113~~ or a polynucleotide sequence of claim 1 or claim 2; wherein said promoter sequence possesses vascular tissue-specific promoter function of the *E. grandis* cOMT gene.

5. (Original) The genetic construct of claim 4, wherein the DNA sequence of interest is operably linked to the promoter in an antisense orientation.

6. (Original) The genetic construct of claim 4, wherein the DNA sequence of interest is a coding sequence operably linked to the promoter in a sense orientation.

7. (Original) The genetic construct of claim 4, wherein the DNA sequence of interest is a coding sequence present in sense and antisense orientations in the construct.

8. (Original) The genetic construct of claim 4, wherein the DNA sequence of interest comprises a non-coding sequence operably linked to the promoter in a sense orientation.

9. (Currently amended) A genetic construct comprising in the 5'-3' direction:

(a) a promoter sequence;

(b) a polynucleotide sequence ~~comprising a functional vascular tissue-specific *E. grandis* cOMT promoter contained in SEQ ID NO: 113~~ or a polynucleotide sequence of claim 1 or 2; and

(c) a gene termination sequence,

wherein the promoter sequence in (a) comprises a xylem-specific promoter sequence that is different from the polynucleotide sequence of (b), ~~and said polynucleotide sequence of (b) is inserted in said construct as a direct or inverted repeat.~~

10. (Currently amended) A host cell comprising the genetic construct of claims 4, 8 ~~and~~ or 9.

11. (Previously presented) The host cell of claim 10, wherein the host cell is a plant cell.

Claims 12-14. (Cancelled).

15. (Currently amended) A method for identifying a gene responsible for a desired function or phenotype, comprising:

(a) transforming a plant cell with a genetic construct comprising a polynucleotide sequence ~~comprising a functional vascular tissue specific *E. grandis* cOMT promoter contained in SEQ ID NO: 113 or a polynucleotide sequence of claim 1 or 2;~~

(b) cultivating the plant cell under conditions conducive to regeneration and mature plant growth to provide a transgenic plant; and

(c) comparing the phenotype of the transgenic plant with the phenotype of a non-transformed plant, wherein said transgenic plant possesses the desired phenotype resulting from a change in lignification as compared to said non-transformed plant; and

wherein the gene encodes a polypeptide involved in secondary cell wall formation.

16. (New) The method of claim 15, wherein said lignification is reduced in said transgenic plant as compared to said non-transformed plant.

17. (New) The genetic construct of claim 9, wherein said polynucleotide sequence of (b) is inserted in said construct as a direct or inverted repeat.

18. (New) An isolated polynucleotide sequence comprising a sequence selected from the group consisting of:

a polynucleotide comprising a 20-mer, a 40-mer, a 60-mer, an 80-mer, a 100-mer, a 120-mer, a 150-mer, a 180-mer, a 220-mer, a 250-mer, a 300-mer, 400-mer, 500-mer or 600-mer of a sequence recited in claim 1 or claim 2.